

AMENDMENTS TO THE DRAWINGS

Please replace the drawings with the attached formal drawing sheets (forty-six (46) different sheets, Figs. 1A-9E) submitted herewith.



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

Docket No. 28110/36120C

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ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60
ATGTGCTTTT TAAATTGGCC TGGGTGACCC GCCCACTTGG TGTAAAAGAA GAACCGGCCA 120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC 180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25
CAG ACC TGG TTT GAA GGT GTC TTC TTT TCC ATG TGC CCC ATT AAT 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55
GGA GCT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

FIG. 1A



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ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt	471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu	
75	80
	85
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu	
90	95
	100
	105
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110	115
	120
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125	130
	135
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Glu Val Glu Glu Ile Phe Lys Asn	
140	145
	150
TCA CCT TTC CTG GTC CCA GAT GGC AGC AGC GTT AGC ATC ATG GAT GGG TCC	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155	160
	165

FIG. 1B



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TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759
Tyr Glu Gly Ile Leu Ala 175	
170	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807
Leu His Gly Arg Gly Gln 190	
195	
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	
205	
210	
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	
220	
225	
230	
TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	
235	
240	
245	
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	
250	
255	
260	
265	

FIG. 1C



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ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	270 275 280
TTT GGG GGT GTG AAA TAC CAG CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG	1095
Phe Gly Gly Val Lys Tyr Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met	285 290 295
GGC TTT GAA CCC TGC TAT TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA	1143
Gly Phe Glu Pro Cys Tyr Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	300 305 310
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	315 320 325
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC CAC TTG ATC GAT TAT GAA AAG	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	330 335 340 345
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	350 355 360

FIG. 1D



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TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG	1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Ser Gly Ser Pro Phe Leu Cys Met	375
	370
	365
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	390
	385
	380
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC	1431
Glu Arg His Pro Leu Thr Ala Thr Ala His Lys Lys Glu Ser Glu Gln His Arg Asp	405
	400
	395
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT	1479
Trp Leu Gly Leu Gly His Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His	425
	415
	410
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA	1527
His Gln Leu Arg Pro Ser Ser Thr Thr Ser Ser Glu Ala Cys Ile Ser Glu Pro	440
	430
	435
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT	1575
Val Phe Ser Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	455
	445
	450

FIG. 1E



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GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT 1629
Gly Lys Ala Trp Pro Glu Thr Arg
460 465

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTGCA CATCTAATGT 1689

GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTTGGGA 1749

TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT 1809

TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAT CTCGTTTCAA CCCTTGGATG 1869

CCTCATTTGCT TTGAATGGAT TCATTTTTCG TTATAAGCTG ATTTACTGAA ATCCCATAAC 1929

CCATCAATGC TGTTAATTTT TTTCTTCCTA CCCTTATTAC ATCCCTACC CTAAAAGCCT 1989

GGGGGAAATA CCTGGTTTTC CTTCCTCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT 2049

GTATTAGAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA 2109

AAAAAAAAAA 2119

FIG. 1F



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peaNTase	1	- - - M <u>E</u> L <u>I</u> K <u>L</u> I <u>T</u> F <u>L</u> L <u>F</u> S <u>M</u> P <u>A</u> I <u>T</u> S <u>S</u> Q <u>Y</u> L <u>G</u> N <u>N</u> L <u>L</u> T <u>S</u> R <u>K</u> I <u>F</u> L <u>K</u> Q <u>E</u> E <u>I</u> S <u>S</u> Y <u>A</u> V <u>V</u> F <u>D</u> A <u>G</u> S <u>T</u> G <u>S</u> R
potapyrase	1	M <u>L</u> N <u>Q</u> N <u>S</u> H <u>F</u> I <u>F</u> I <u>L</u> A <u>I</u> F <u>L</u> V <u>L</u> P <u>L</u> S <u>L</u> S <u>K</u> N <u>V</u> N <u>A</u> Q <u>I</u> P <u>L</u> R <u>R</u> H <u>L</u> L <u>S</u> H <u>E</u> S <u>E</u> - - H <u>Y</u> A <u>V</u> I <u>F</u> D <u>A</u> G <u>S</u> T <u>G</u> S <u>R</u>
mNTase	1	M <u>A</u> T <u>S</u> W <u>G</u> A <u>V</u> F <u>M</u> L <u>I</u> I <u>A</u> C <u>V</u> G <u>S</u> T <u>V</u> F <u>Y</u> R <u>E</u> Q <u>Q</u> T <u>W</u> F <u>E</u> G <u>V</u> F <u>L</u> S <u>S</u> M <u>C</u> P <u>I</u> N <u>V</u> S <u>A</u> G <u>T</u> F <u>Y</u> G <u>I</u> M <u>F</u> D <u>A</u> G <u>S</u> T <u>G</u> T <u>R</u>
yGDPase	1	K <u>T</u> P <u>E</u> D <u>I</u> S <u>I</u> L <u>P</u> V <u>N</u> D <u>E</u> P <u>G</u> Y <u>L</u> Q <u>D</u> S <u>K</u> T <u>E</u> Q <u>N</u> Y <u>P</u> E <u>L</u> A <u>D</u> A <u>V</u> K <u>S</u> T <u>S</u> Q <u>T</u> C <u>S</u> E <u>H</u> K <u>Y</u> V <u>I</u> M <u>I</u> D <u>A</u> G <u>S</u> T <u>G</u> S <u>R</u>
peaNTase	57	I <u>H</u> V <u>Y</u> H <u>F</u> N <u>Q</u> N <u>D</u> L <u>L</u> H <u>I</u> G <u>K</u> G <u>V</u> E <u>Y</u> N <u>K</u> I <u>T</u> P <u>G</u> L <u>S</u> S <u>Y</u> A <u>N</u> N <u>P</u> E <u>Q</u> A <u>A</u> K <u>S</u> L <u>I</u> P <u>L</u> L <u>E</u> Q <u>A</u> E <u>D</u> V <u>V</u> P <u>D</u> D <u>L</u> Q <u>P</u>
potapyrase	59	V <u>H</u> V <u>F</u> R <u>F</u> D <u>E</u> K <u>L</u> G <u>L</u> L <u>P</u> I <u>G</u> N <u>N</u> I <u>E</u> Y <u>F</u> M <u>A</u> T <u>E</u> P <u>G</u> L <u>S</u> S <u>Y</u> A <u>E</u> D <u>P</u> K <u>A</u> A <u>N</u> S <u>L</u> E <u>P</u> L <u>L</u> D <u>G</u> A <u>E</u> G <u>V</u> V <u>P</u> Q <u>E</u> L <u>Q</u> S
mNTase	61	I <u>H</u> V <u>Y</u> T <u>F</u> V <u>Q</u> K <u>T</u> A <u>G</u> Q <u>L</u> P <u>F</u> L <u>E</u> G <u>E</u> I <u>F</u> D <u>S</u> V <u>K</u> P <u>G</u> L <u>S</u> A <u>F</u> V <u>D</u> Q <u>P</u> K <u>Q</u> G <u>A</u> E <u>T</u> V <u>Q</u> E <u>L</u> L <u>E</u> V <u>A</u> K <u>D</u> S <u>I</u> P <u>R</u> S <u>H</u> W <u>E</u>
yGDPase	61	V <u>H</u> I <u>Y</u> K <u>F</u> D <u>V</u> C <u>T</u> S - - P <u>P</u> T <u>L</u> L <u>D</u> E <u>K</u> F <u>D</u> M <u>L</u> E <u>P</u> G <u>L</u> S <u>S</u> F <u>D</u> T <u>D</u> S <u>V</u> G <u>A</u> A <u>N</u> S <u>L</u> D <u>P</u> L <u>L</u> K <u>V</u> A <u>M</u> N <u>Y</u> V <u>P</u> I <u>K</u> A <u>R</u> S
peaNTase	117	K <u>T</u> P <u>V</u> R <u>L</u> G <u>A</u> T <u>A</u> G <u>L</u> R <u>L</u> L <u>N</u> G <u>D</u> A <u>S</u> E <u>K</u> I <u>L</u> Q <u>S</u> V <u>R</u> D <u>M</u> L <u>S</u> N <u>R</u> S <u>T</u> F - N <u>V</u> Q <u>P</u> D <u>A</u> V <u>S</u> I <u>I</u> D <u>G</u> T <u>Q</u> E <u>G</u> S <u>Y</u> L <u>W</u> V <u>T</u>
potapyrase	119	E <u>T</u> P <u>L</u> E <u>L</u> G <u>A</u> T <u>A</u> G <u>L</u> R <u>M</u> L <u>K</u> G <u>D</u> A <u>A</u> E <u>K</u> I <u>L</u> Q <u>A</u> V <u>R</u> N <u>L</u> V <u>K</u> N <u>Q</u> S <u>T</u> F - H <u>S</u> K <u>D</u> Q <u>W</u> V <u>T</u> I <u>L</u> D <u>G</u> T <u>Q</u> E <u>G</u> S <u>Y</u> M <u>W</u> A <u>A</u>
mNTase	121	R <u>T</u> P <u>V</u> V <u>L</u> K <u>A</u> T <u>A</u> G <u>L</u> R <u>L</u> L <u>P</u> E <u>Q</u> K <u>A</u> Q <u>A</u> L <u>L</u> L <u>E</u> V <u>E</u> E <u>I</u> F <u>K</u> N - S <u>P</u> F - L <u>V</u> P <u>D</u> G <u>S</u> V <u>S</u> I <u>M</u> D <u>G</u> S <u>Y</u> E <u>G</u> I <u>L</u> A <u>W</u> V <u>T</u>
yGDPase	119	C <u>T</u> P <u>V</u> A <u>V</u> K <u>A</u> T <u>A</u> G <u>L</u> R <u>L</u> L <u>G</u> D <u>A</u> K <u>S</u> S <u>K</u> I <u>L</u> S <u>A</u> V <u>R</u> D <u>H</u> L <u>E</u> K <u>D</u> Y <u>P</u> F <u>P</u> V <u>E</u> G <u>D</u> G <u>V</u> S <u>I</u> M <u>G</u> G <u>D</u> E <u>E</u> G <u>V</u> F <u>A</u> W <u>I</u> T

FIG. 2A



Title: METHODS AND COMPOSITIONS
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peaNTase	176	<u>VNYALGNLGKKYTK</u> - - <u>TVGVIDLGGGSVQMAYAVSKK</u> <u>TAKNAPKVADGDDPYIKKVVVLKG</u>
potapyrase	178	<u>INYLLGNLGKDYKS</u> - - <u>TTATIDLGGGSVQMAYAISNEQFAKAPQNE</u> <u>DG-EPYVQQKHLMS</u>
mNTase	179	<u>VNFLTGQLHGRGQE</u> - - <u>TVGTLDLGGASTOITFLPQFEK</u> - - - - <u>TLEQTPRGYLTSEMFN</u>
YGDPase	179	<u>TNYLLGNIGANGPKLP</u> <u>TAAVFDLGGGSTQIVFEP</u> - - <u>TFPINEKMOV</u> <u>DGEHKF</u> - - <u>DLKFGD</u>
peaNTase	234	<u>IPYDLYVHSYLFHFGREASRAEILKL</u> - - - - - <u>TPRSPNPCLLAGFN</u> <u>GIY</u>
potapyrase	235	<u>KDYNLYVHSYLYNYGQLAGRAEIFKA</u> - - - - - <u>SRNESNPCALEGCDGY</u>
mNTase	232	<u>STFKLYTHSYLGFGLKAARLATLGA</u> - - - - - <u>LEAKGT</u> - - - - <u>DGHTFRS</u>
YGDPase	234	<u>ENYTLYQF</u> <u>SHLGYGLKEGRNKVNSVL</u> <u>VENALKDGI</u> <u>LKGDNTKTHQLSSPC</u> <u>LPKVNATN</u>
peaNTase	276	<u>TYSGE</u> <u>EFKATA</u> <u>YTS</u> <u>GA</u> - - - - - <u>NFNKCKNTIRKALKLNYP</u> <u>CPYQ</u> <u>NC</u> <u>TFGGI</u> <u>WNGGGN</u> - - -
potapyrase	277	<u>SYGGVDYKVKAPKKGS</u> - - - - - <u>SWKRCRRLTRHALKINAKCNIE</u> <u>ECTF</u> <u>NGVW</u> <u>NGGGD</u> - - -
mNTase	270	<u>ACLPRWLEAEWIFGGV</u> - - - - - <u>KYQYGGNQEGEMGF</u> <u>PCYAE</u> <u>VL</u> <u>VQ</u> <u>KL</u> <u>HQ</u> <u>PEEV</u> <u>R</u> - - -
YGDPase	294	<u>EKV</u> <u>TL</u> <u>ESKE</u> <u>TY</u> <u>TID</u> <u>FIG</u> <u>DP</u> <u>ES</u> <u>GA</u> <u>QC</u> <u>RF</u> <u>LT</u> <u>DE</u> <u>IL</u> <u>NK</u> <u>DA</u> <u>QC</u> <u>QS</u> <u>PP</u> <u>CS</u> <u>FN</u> <u>GV</u> <u>HQ</u> <u>PS</u> <u>LV</u> <u>RT</u> <u>FK</u>

FIG. 2B



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peaNTase	328	<u>GQKNLFASSFFYL</u> <u>PEDTGMVDA</u> <u>STPNFIL</u> <u>RPVDIET</u> <u>KAKEACALNF</u> <u>EDAKSTYP</u> <u>FLD</u> <u>KK</u>
potapyrase	329	<u>GQKNIHASSFFYD</u> <u>IGAQVGIVD</u> <u>TKFPSA</u> <u>LAKPIQY</u> <u>LNAAKVA</u> <u>CQTNVAD</u> <u>IKSIF</u> <u>PKTQDR</u>
mNTase	322	<u>GSA-FYA</u> <u>FSYYDRAAD</u> <u>THLIDYE</u> <u>-KGGV</u> <u>LKVED</u> <u>FERKARE</u> <u>VCD-N</u> <u>LGSFSS</u> <u>GSP----</u>
YGDPase	354	<u>ESNDIYI</u> <u>FSYFYDR</u> <u>TRPLG</u> <u>MPLSFT</u> <u>LNELND</u> <u>LARI</u> <u>IVCKGE</u> <u>ETWNSV</u> <u>FSGI</u> <u>AGS---</u> <u>LDEL</u>
peaNTase	388	<u>NVASYV</u> <u>CMDLIYQY</u> <u>VLLVD</u> <u>GGFGLD</u> <u>PLQKIT</u> <u>SGKEI</u> <u>EYQDAI</u> <u>VEAAW</u> <u>PLGNA</u> <u>VEA</u> <u>ISAL</u> <u>PK</u>
potapyrase	389	<u>NI-PY</u> <u>LCMDLI</u> <u>YEY</u> <u>TLLVD</u> <u>GGFGLN</u> <u>PHKEI</u> <u>TVIH</u> <u>DVQY</u> <u>KNYLV</u> <u>GAAW</u> <u>PLGCA</u> <u>IDLV</u> <u>SS</u> <u>TN</u>
mNTase	374	<u>-----</u> <u>FLC</u> <u>MDLT</u> <u>YIT</u> <u>ALLK</u> <u>DGLG</u> <u>FAER</u> <u>HPLT</u> <u>AHKE</u> <u>SEQH</u> <u>RDWL</u> <u>GLGG</u> <u>HLS</u> <u>PAPV</u> <u>SGH</u> <u>QLR</u>
YGDPase	411	<u>ESDSH</u> <u>FC</u> <u>LDL</u> <u>SFQV</u> <u>SLLH</u> <u>TGYD</u> <u>IPLQ</u> <u>REL</u> <u>RTG</u> <u>KKI</u> <u>ANKE---</u> <u>IGW</u> <u>CLGAS</u> <u>LP</u> <u>LLK</u> <u>ADNW</u>
peaNTase	448	<u>F</u> <u>ER</u> <u>L</u> <u>M</u> <u>Y</u> <u>F</u> <u>V</u>
potapyrase	448	<u>K</u> <u>I</u> <u>R</u> <u>V</u> <u>A</u> <u>S</u> <u>S</u> <u>*</u>
mNTase	430	<u>P</u> <u>S</u> <u>S</u> <u>T</u> <u>S</u> <u>E</u> <u>A</u> <u>C</u> <u>I</u> <u>S</u> <u>E</u> <u>P</u> <u>V</u> <u>F</u> <u>S</u> <u>Q</u> <u>E</u> <u>G</u> <u>V</u> <u>D</u> <u>S</u> <u>E</u> <u>T</u> <u>F</u> <u>S</u> <u>D</u> <u>L</u> <u>S</u> <u>G</u> <u>K</u> <u>A</u> <u>W</u> <u>P</u> <u>E</u> <u>T</u> <u>R</u> <u>*</u>
YGDPase	467	<u>K</u> <u>C</u> <u>K</u> <u>I</u> <u>Q</u> <u>S</u> <u>A</u>

FIG. 2C



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		ACRI	
CD39	1	VKYGIVL	DAGSSHTS
ratCD39	1	VKYGIVL	DAGSSHTN
CD39L1	1	LKYGIVL	DAGSSHTS
chiATPase	1	FKYGIVL	DAGSSHTA
peaNTase	1	SSYAVVF	DAGSTGSR
potRRP1	1	EHYAVIF	DAGSTGSR
YGDA1	1	HKYVIMI	DAGSTGSR
mNTase	1	TFYGIMF	DAGSTGTR
hCD39L2	1		
celegans	1	IKYGVIC	DAGSSGTR
Y71KD	1	DRFGIVI	DAGSSGSR

LYIYKW	PAEKENDTGV	VHQVEECRVK	GPGIS
LYIYKW	PAEKENDTGV	VQLLEECQVK	GPGIS
MFYIKW	PADKENDTGI	VQGHSSCDVP	GGGIS
VFIYKW	PADKENDTGV	VSEHSMCDVE	GPGIS
IHVYHF	NQ-NLDLLHIGKGV	YNN	KITPGLS
VHVFRF	DE-KLGLLPIGNNIE	YFM	ATEPGLS
VHIYKF	DVCTSP	PTLLD-EKFD	MLEPGLS
IHVYTF	VQKTAGQLPFL	EG-EIFD	SVKPGLS
		FK	ALKPGLS
LFVYTLKPLSGGL	TNIDT	L	IHESEPVKKVT
IHVFKWQDTE	SLHATNQDSQ	SILQSVPHIHQEKD	WTFKLN

FIG. 3A



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

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ACR II

CD39	47	<u>K</u> <u>F</u> - <u>V</u> <u>Q</u> <u>K</u> <u>V</u> <u>N</u> <u>E</u> <u>I</u> <u>G</u> <u>I</u> - <u>Y</u> <u>L</u> <u>T</u> <u>D</u> <u>C</u> <u>M</u> <u>E</u> <u>R</u> <u>A</u> <u>R</u> <u>E</u> <u>V</u> <u>I</u> <u>P</u> <u>R</u> - - - <u>S</u> - <u>Q</u> <u>H</u> <u>Q</u> <u>E</u> <u>T</u> <u>P</u> <u>V</u> <u>Y</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> <u>R</u> <u>M</u> <u>E</u> <u>S</u> <u>E</u> <u>E</u> <u>L</u> <u>A</u> <u>D</u>
ratCD39	47	<u>K</u> <u>Y</u> - <u>A</u> <u>Q</u> <u>K</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>A</u> <u>A</u> - <u>Y</u> <u>L</u> <u>A</u> <u>E</u> <u>C</u> <u>M</u> <u>K</u> <u>M</u> <u>S</u> <u>T</u> <u>E</u> <u>R</u> <u>I</u> <u>P</u> <u>A</u> - - - <u>S</u> <u>K</u> <u>Q</u> <u>H</u> <u>Q</u> - <u>T</u> <u>P</u> <u>V</u> <u>Y</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> <u>R</u> <u>M</u> <u>E</u> <u>S</u> <u>K</u> <u>Q</u> <u>S</u> <u>A</u> <u>D</u>
CD39L1	47	<u>S</u> <u>Y</u> - <u>A</u> <u>D</u> <u>N</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>S</u> <u>Q</u> - <u>S</u> <u>L</u> <u>V</u> <u>G</u> <u>C</u> <u>L</u> <u>E</u> <u>Q</u> <u>A</u> <u>L</u> <u>Q</u> <u>D</u> <u>V</u> <u>P</u> <u>K</u> - - - <u>E</u> <u>R</u> - <u>H</u> <u>A</u> <u>G</u> <u>T</u> <u>P</u> <u>L</u> <u>Y</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> <u>N</u> <u>L</u> <u>T</u> <u>N</u> <u>P</u> <u>E</u> <u>A</u> <u>S</u> <u>T</u>
chiATPase	47	<u>S</u> <u>Y</u> - <u>S</u> <u>S</u> <u>K</u> <u>P</u> <u>P</u> <u>A</u> <u>A</u> <u>G</u> <u>K</u> - <u>S</u> <u>L</u> <u>E</u> <u>H</u> <u>C</u> <u>L</u> <u>S</u> <u>Q</u> <u>A</u> <u>M</u> <u>R</u> <u>D</u> <u>V</u> <u>P</u> <u>K</u> - - - <u>E</u> <u>K</u> - <u>H</u> <u>A</u> <u>D</u> <u>T</u> <u>P</u> <u>L</u> <u>Y</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> <u>T</u> <u>I</u> <u>A</u> <u>D</u> <u>P</u> <u>P</u> <u>S</u> <u>Q</u> <u>T</u>
peaNTPase	46	<u>S</u> <u>Y</u> - <u>A</u> <u>N</u> <u>N</u> <u>P</u> <u>E</u> <u>Q</u> <u>A</u> <u>A</u> <u>K</u> <u>S</u> - <u>L</u> <u>I</u> <u>P</u> <u>L</u> <u>L</u> <u>E</u> <u>Q</u> <u>A</u> <u>E</u> <u>D</u> <u>V</u> <u>V</u> <u>P</u> - - - <u>D</u> <u>D</u> <u>L</u> <u>Q</u> <u>P</u> <u>K</u> <u>T</u> <u>P</u> <u>V</u> <u>R</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>R</u> <u>L</u> <u>L</u> <u>N</u> - - - <u>G</u> <u>D</u> <u>A</u> - <u>S</u> <u>E</u>
potRRP1	46	<u>S</u> <u>Y</u> - <u>A</u> <u>E</u> <u>D</u> <u>P</u> <u>K</u> <u>A</u> <u>A</u> <u>N</u> <u>S</u> - <u>L</u> <u>E</u> <u>P</u> <u>L</u> <u>L</u> <u>D</u> <u>G</u> <u>A</u> <u>E</u> <u>G</u> <u>V</u> <u>V</u> <u>P</u> - - - <u>Q</u> <u>E</u> <u>L</u> <u>Q</u> <u>S</u> <u>E</u> <u>T</u> <u>P</u> <u>L</u> <u>E</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>R</u> <u>M</u> <u>L</u> <u>K</u> - - - <u>G</u> <u>D</u> <u>A</u> - <u>A</u> <u>E</u>
YGDA1	44	<u>S</u> <u>P</u> <u>D</u> <u>T</u> <u>D</u> <u>S</u> <u>V</u> - <u>G</u> <u>A</u> <u>A</u> <u>N</u> <u>S</u> - <u>L</u> <u>D</u> <u>P</u> <u>L</u> <u>L</u> <u>K</u> <u>V</u> <u>A</u> <u>M</u> <u>N</u> <u>Y</u> <u>V</u> <u>P</u> <u>I</u> - - - <u>K</u> <u>A</u> <u>R</u> <u>S</u> <u>C</u> <u>T</u> <u>P</u> <u>V</u> <u>A</u> <u>V</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>R</u> <u>L</u> <u>L</u> - - - <u>G</u> <u>D</u> <u>A</u> <u>K</u> <u>S</u>
mNTPase	46	<u>A</u> <u>F</u> - <u>V</u> <u>D</u> <u>Q</u> <u>P</u> <u>K</u> <u>Q</u> <u>G</u> <u>A</u> <u>E</u> <u>T</u> - <u>V</u> <u>Q</u> <u>E</u> <u>L</u> <u>L</u> <u>E</u> <u>V</u> <u>A</u> <u>K</u> <u>D</u> <u>S</u> <u>I</u> <u>P</u> <u>R</u> <u>S</u> <u>H</u> <u>W</u> <u>E</u> - - - <u>R</u> - <u>T</u> <u>P</u> <u>V</u> <u>V</u> <u>L</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>R</u> <u>L</u> <u>L</u> - - - <u>P</u> <u>E</u> <u>Q</u> <u>K</u> <u>A</u> <u>Q</u>
hCD39L2	10	<u>A</u> <u>Y</u> - <u>A</u> <u>D</u> <u>D</u> <u>V</u> <u>E</u> <u>K</u> <u>S</u> <u>A</u> <u>Q</u> <u>G</u> - <u>I</u> <u>R</u> <u>E</u> <u>L</u> <u>L</u> <u>D</u> <u>V</u> <u>A</u> <u>K</u> <u>D</u> <u>I</u> <u>P</u> - - - <u>F</u> <u>D</u> <u>S</u> <u>G</u> <u>R</u> <u>P</u> - <u>T</u> <u>P</u> <u>L</u> <u>V</u> <u>L</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>R</u> <u>L</u> <u>L</u> - - - <u>P</u> <u>G</u> <u>E</u> <u>K</u> <u>A</u> <u>Q</u>
celegans	51	<u>S</u> <u>F</u> <u>G</u> - <u>D</u> <u>K</u> <u>P</u> <u>E</u> <u>Q</u> <u>V</u> <u>V</u> <u>E</u> - <u>Y</u> <u>L</u> <u>T</u> <u>P</u> <u>L</u> <u>L</u> <u>R</u> <u>F</u> <u>A</u> <u>E</u> <u>E</u> <u>H</u> <u>I</u> <u>P</u> <u>Y</u> <u>E</u> <u>Q</u> <u>L</u> <u>G</u> <u>E</u> - - - <u>T</u> <u>D</u> <u>L</u> <u>L</u> <u>I</u> <u>F</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> - - - <u>P</u> <u>E</u> <u>A</u> <u>Q</u> <u>K</u> <u>D</u>
y71KD	61	<u>S</u> <u>P</u> <u>E</u> - <u>K</u> <u>K</u> <u>P</u> <u>Q</u> <u>D</u> <u>A</u> <u>Y</u> <u>K</u> <u>S</u> <u>H</u> <u>I</u> <u>K</u> <u>P</u> <u>L</u> <u>L</u> <u>D</u> <u>F</u> <u>A</u> <u>K</u> <u>N</u> <u>I</u> <u>I</u> <u>P</u> <u>E</u> <u>S</u> <u>H</u> <u>W</u> <u>S</u> - - - <u>C</u> <u>P</u> <u>V</u> <u>F</u> <u>I</u> <u>Q</u> <u>A</u> <u>T</u> <u>A</u> <u>G</u> <u>M</u> <u>R</u> <u>L</u> <u>L</u> - - - <u>P</u> <u>Q</u> <u>D</u> <u>I</u> <u>Q</u> <u>S</u>

FIG. 3B



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

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		ACR III									
CD39	101	<u>RVLDVVERSLN</u> - <u>YPP</u> - - - - <u>DFQGARII</u> <u>TGEEGAYGWITIN</u> <u>YLLGKFSQKTRWFSI</u> <u>VP</u>									
ratCD39	101	<u>EVLAASVRSLSKS</u> - <u>YPP</u> - - - - <u>DFQGA</u> <u>KIITGQEEGAYGWITIN</u> <u>YLLGRFTQEQSWLNFIS</u>									
CD39L1	101	<u>SVLMAVTHLTQ</u> - <u>YPP</u> - - - - <u>DFRGARILS</u> <u>GQEEGVFGWVTAN</u> <u>YLLENFI</u> - <u>KYGWVG</u> - - <u>R</u>									
chiATPase	101	- <u>CLSAVMATLKS</u> - <u>YPP</u> - - - - <u>DFGGAKILS</u> <u>GEEGVFGWITAN</u> <u>YLLENFI</u> - <u>KRGWLG</u> - - <u>E</u>									
peaNTase	97	<u>KILQSVRDMLSNRSTFN</u> - <u>VQPD</u> - <u>A</u> - <u>VSIIDGTQEGSYLWVTVN</u> <u>YALGN</u> - - - - - <u>L</u> - - - <u>G</u>									
potRRP1	97	<u>KILQAVRNLVKNQSTFH</u> - - <u>SKD</u> - <u>QWVTILDGTQEGSYMWA</u> <u>AINYLLGN</u> - - - - - <u>L</u> - - - <u>G</u>									
YGDA1	95	<u>KILSAVRDHL</u> <u>EKDYPPVVEGD</u> - <u>G</u> - <u>VSIMGGDEGVFAWIT</u> <u>NYLLGN</u> - - - - - <u>IGANG</u>									
mNTase	97	<u>ALLLEVEEIF</u> - <u>KNSPF</u> - <u>LV</u> - <u>PD</u> - <u>GSVSIMDGS</u> <u>YEGILAWVTVN</u> <u>FLTGTQ</u> - - - - - <u>LHGRG</u>									
hCD39L2	61	<u>KLLQKVKEYL</u> - <u>KHSPP</u> - <u>LV</u> - <u>GD</u> - <u>DCVSIMNGTDEGVSAWXTIN</u> <u>FLTGS</u> - - - - - <u>LKTPG</u>									
celegans	102	<u>AIKKNLQNGLSVTALRVSD</u> - - - <u>SNIRIIDGAWEGIYSWIAVN</u> <u>YILGR</u> - - - - - <u>F</u> - <u>D</u> - -									
Y71KD	113	<u>SILDGLCQGLKHPA</u> <u>EFLVEDCS</u> - <u>AQIQVIDGETEGLYGWLGL</u> <u>NYLYGH</u> - - - - - <u>FNDYN</u>									

FIG. 3C



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

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		ACR IV	
CD39	155	<u>Y</u> <u>E</u> <u>T</u> <u>N</u> <u>N</u> <u>Q</u> <u>E</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>Q</u> <u>N</u> <u>Q</u>	
ratCD39	155	- <u>D</u> <u>S</u> <u>Q</u> <u>K</u> <u>Q</u> <u>A</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>S</u> <u>T</u> <u>Q</u> <u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>L</u> <u>N</u> <u>Q</u>	
CD39L1	152	<u>W</u> <u>P</u> <u>R</u> <u>P</u> <u>R</u> <u>K</u> <u>G</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>T</u> <u>S</u> <u>P</u>	
chiATPase	151	<u>W</u> <u>I</u> <u>Q</u> <u>S</u> <u>K</u> <u>K</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u> <u>F</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>S</u> <u>D</u> <u>A</u> <u>I</u>	
peaNTPase	144	<u>K</u> <u>K</u> <u>Y</u> <u>T</u> <u>K</u> - - <u>T</u> <u>V</u> <u>G</u> <u>V</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>V</u> <u>S</u> <u>K</u> <u>K</u>	
potRROP1	144	<u>K</u> <u>D</u> <u>Y</u> <u>K</u> <u>S</u> - - <u>T</u> <u>T</u> <u>A</u> <u>T</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>I</u> <u>S</u> <u>N</u> <u>E</u>	
YGDA1	146	<u>P</u> <u>K</u> <u>L</u> - <u>P</u> - - <u>T</u> <u>A</u> <u>A</u> <u>V</u> <u>F</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>V</u> <u>F</u> <u>E</u> <u>P</u> <u>T</u> <u>F</u> <u>P</u> <u>I</u>	
mNTPase	146	<u>Q</u> <u>E</u> - - - - <u>T</u> <u>V</u> <u>G</u> <u>T</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>L</u> <u>P</u> <u>Q</u> <u>F</u> <u>E</u>	
hCD39L2	110	<u>G</u> <u>S</u> - - - - <u>S</u> <u>V</u> <u>G</u> <u>M</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> <u>L</u> <u>P</u> <u>R</u> <u>V</u> <u>E</u>	
celegans	149	<u>K</u> <u>E</u> - <u>N</u> <u>D</u> <u>S</u> - <u>K</u> <u>V</u> <u>G</u> <u>M</u> <u>I</u> <u>D</u> <u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>V</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> <u>E</u> <u>I</u> <u>A</u> - <u>N</u> <u>E</u>	
y71KD	165	<u>P</u> <u>E</u> <u>V</u> <u>S</u> <u>D</u> <u>H</u> <u>F</u> <u>T</u> <u>F</u> <u>G</u> <u>F</u> <u>M</u> <u>D</u> <u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> - - <u>A</u> <u>P</u> <u>H</u> <u>D</u> <u>S</u>	

FIG. 3D



Title: METHODS AND COMPOSITIONS
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GTGGGGTCGT	ATCCCCGCGG	TGGAGGCCGG	GGTGGGCCGG	GCCGGGGCGG	GGGAGCCCAA	60	
AAGACCGGCT	GCCGCCCTGCT	CCCCGGAAAA	GGCACTCGT	CTCCGTGGGT	GTGGCGGAGC	120	
GCGCGGTGCA	TGGAATGGGC	TATGTGAATG	AAAAAAGGTA	TCCGTTATGA	AACTTCCAGA	180	
AAAACGAGCT	ACATTTTTC	GCAGCCGCAG	CACGGTCCTT	GGCAACAAG	G ATG AGA	237	
					Met Arg		
					1		
AAA ATA	TCC AAC	CAC GGG	AGC CTG	CGG GTG	GCG AAG	GTG GCA TAC CCC	285
Lys Ile Ser	Asn His	Gly Ser	Leu Arg	Val Ala	Lys Val	Ala Tyr Pro	
	5		10		15		
CTG GGG	CTG TGT	GTG GGC	GTG GTG	ATC ATC	TAT GGT	GCC TAC ATC AAG TGG	333
Leu Gly Leu	Cys Val	Gly Val	Phe Phe	Ile Tyr	Val Ala	Tyr Ile Lys Trp	
	20		25		30		
CAC CGG	GCC ACC	GCC ACC	CAG GCC	TTC AGC	ATC ACC	AGG GCA GCC	381
His Arg Ala	Thr Ala	Thr Gln	Ala Phe	Phe Ser	Ile Thr	Arg Ala Ala	
	35		40		45		
					50		

FIG. 4A



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CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala	
55	65
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70	80
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85	95
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100	110
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115	120
	125
	130

FIG. 4B



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CTA CTG GAT GTT GCT AAA CAG GAC GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Lys Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4C



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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG	957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln	
230 235 240	
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC	1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	
245 250 255	
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGC CTC GGG CTG ATG TCG GCA	1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala	
260 265 270	
CGC CTG GCG ATC CTG GGC GGC GGC GAG GGC CAG CCT GCT AAG GAT GGA	1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly	
275 280 285 290	
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG	1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	
295 300 305	
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA	1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala	
310 315 320	

FIG. 4D



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AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC	1245
Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn	
325 330 335	
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC	1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
340 345 350	
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG	1341
Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu	
355 360 365 370	
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC	1389
Lys Gly Gly Ser Leu Val Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr	
375 380 385	
GTG TGT CCG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC	1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys	
390 395 400	
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG CAG GAG TTC GGC TTT CCC	1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro	
405 410 415	

FIG. 4E



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AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
420 425 430
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435 440 445 450
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG 1629
Gln Lys Ser Pro Ala Ser 455
CAGTGTCTGT GTGTCTGCAT AAACCCCTCCT GTCCCTGGACG TGACTTCATC CTGAGGAGCC 1689
ACAGCACAGG CCGTGCTGGC ACTTTCIGCA CACTGGCTCT GGGACTTGCA GAAGCCTGG 1749
TGCTGCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809
CCCTGCTCAA TGCCACCTGT CTGCCCTGGG TCCAAGTGGG CAGGACCAGG ACAGAACCAC 1869
AGGCACACAC TGAGGGGGCA GTGTGGCTCC CTGCCTGTCC CATCCCCATG CCCC GTCCGC 1929

FIG. 4F



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GGGGCTGTGG CTGCTGCTGT GCATGTCCCT GCGATGGGAG TCTTGCTCTCC CAGCCTGTCA 1989
GTTTCCTCCC CAGGGCAGAG CTCCCCCTTCC TGCAAGAGTC TGGGAGGCGG TGCAGGCTGT 2049
CCTGGCTGCT CTGGGAAGC CGAGGGACAG CCATAACACC CCCGGGACAG TAGGCTCTGGG 2109
CGGCACCACT GGGAACCTG GACTTGAGTG TGTTTGCTCT TCCTTGGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCTGCT CTCCCTCACAC ATTGTGTGT TTTGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCCCA CCTTTCAGGG AGTCTCCCAG CATGGGCGGA 2289
TGCCGGGCAT GAGCTGCTGT AACTATTG TGGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGGTGC CAAGTGCTTG TGTAGAAACT GTGTTCTGAG CCCCCTTTC TGGACACCAA 2409
CTGTGTCCTG TGAATGTATC GCTACTGTGA GGTGTTCCCC CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGG TCAGCTGAGC CACAGTCCCC GAACCAAGCT CTCGGTGTCT 2529

FIG. 4G



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CGGGCCACCA	TCCGCCCACC	TCGGGCTGAC	CCCACCTCCT	CCATGGACAG	TGTGAGCCCC	2589
GGGCCGTGCA	TCCTGCTCAG	TGTGGCGTCA	GTGTCGGGCG	TGAGCCCCCTT	GAGCTGCTTC	2649
AGTGAATGTA	CAGTGCCCCG	CACGAGCTGA	ACCTCATGTG	TTCCACTCCC	AATAAAAGGT	2709
TGACAGGGGC	TTCTCCTTCA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAA	2762

FIG. 4H



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FIG. 5A

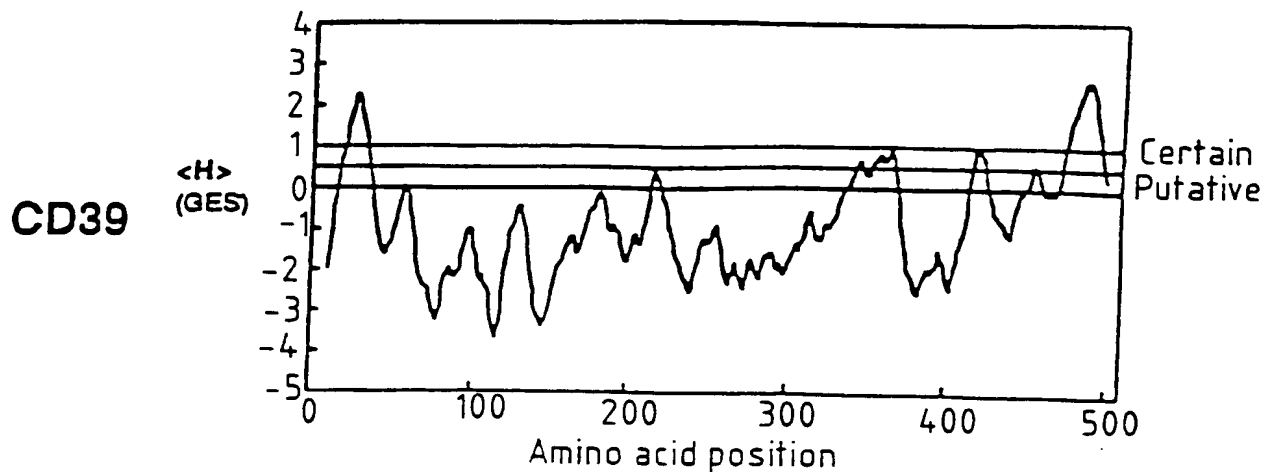


FIG. 5B

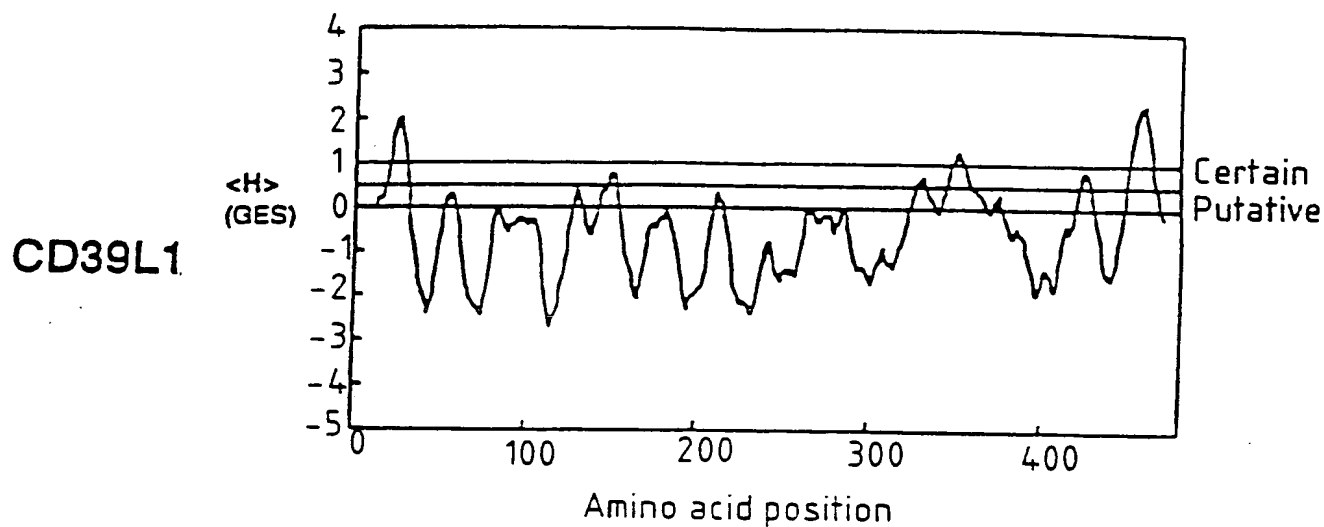
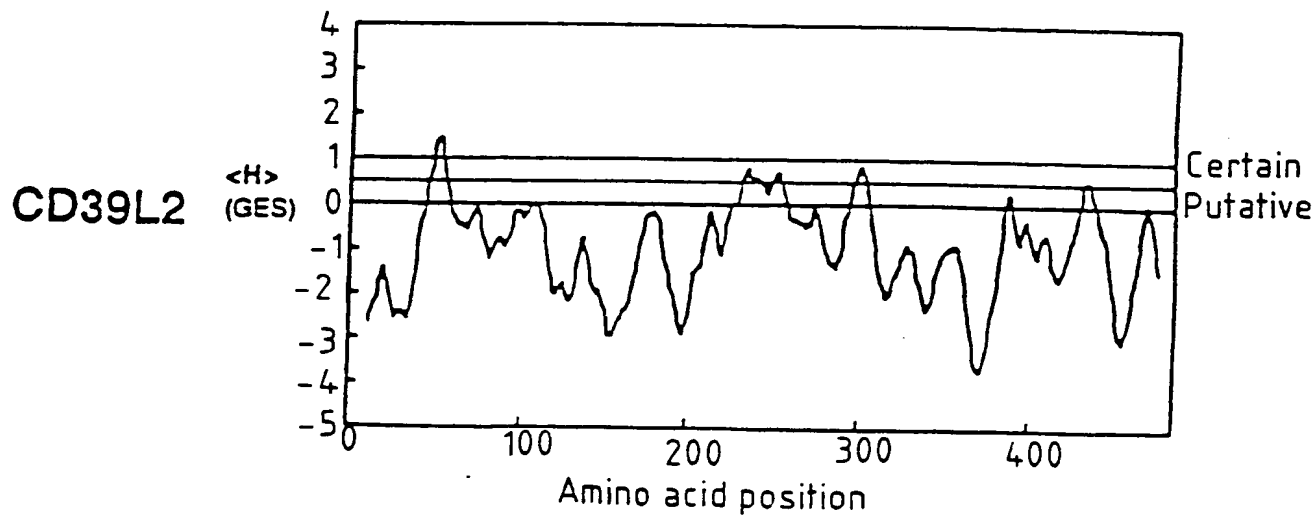
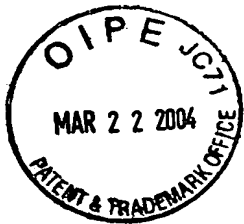


FIG. 5C





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FIG. 5D

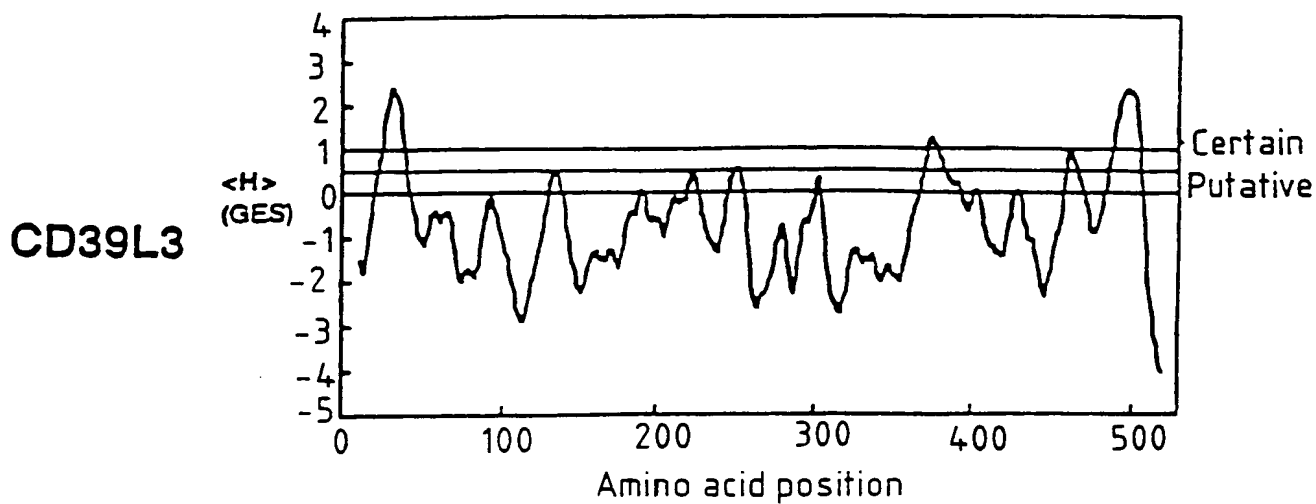
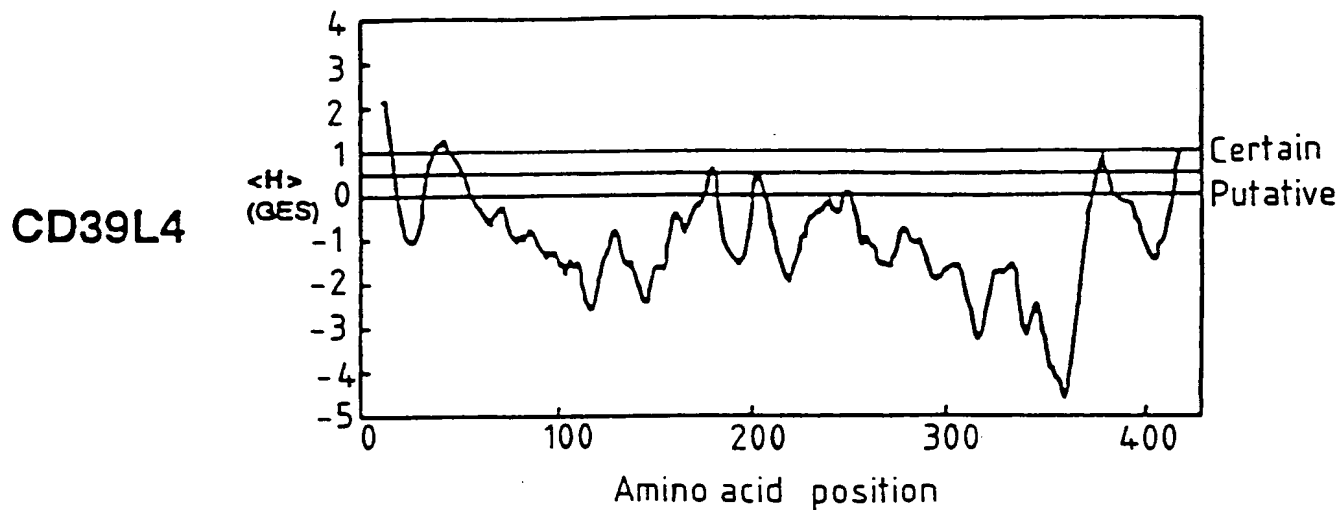
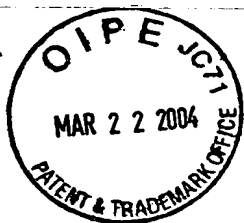


FIG. 5E





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ACCCACGCGT CTGGCCGCGG GCCGCTCTG CGCAGCGGT AGTCGCTTC TCCGAATCGG 60

CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT 112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys 10
1 5

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC 160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala 25
15 20

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC 208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val 40
30 35

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT 256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly 55
45 50

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA 304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln 65
60 70

FIG. 6A



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TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Thr Gly Val Ser Gln Thr Phe	90
75	80
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	105
95	100
caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	120
110	115
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	135
125	130
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	150
140	145
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	170
155	160

FIG. 6B



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TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ser Gly Gln Glu Gly Val Tyr Gly	185
	175
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	200
	190
	195
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	215
	205
	210
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	230
	220
	225
ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	240
	235
	245
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	255
	260
	265

FIG. 6C



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GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	270 275 280
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	285 290 295
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	300 305 310
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	315 320 325 330
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	335 340 345
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	350 355 360

FIG. 6D



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ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT	1216
Ile Lys Gly Pro Phe Val Ala Phe Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	365 370 375
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Ser Leu Asp Thr Phe Asn Ser Ser	380 385 390
ACC TGG AAT TTC TGC TCA GAG AAT TGG AGT CAG CTC CCA CTG CTG CTC	1312
Thr Trp Asn Phe Cys Ser Ser Gln Asn Trp Ser Ser Gln Leu Pro Leu Leu	395 400 405 410
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	415 420 425
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	430 435 440
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	445 450 455

FIG. 6E



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TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	
CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA	1699
Asp His Ala Val Asp Ser Asp	
525	
TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCAATGCA GGTGAAGTGG CTGCCTTCAG	1759

FIG. 6F



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GAAATACAAC TAACTAAAAT CAAACACCTA GGTCACGTGC CTCTCAAATA CTGATTCTG 1819
CCACAGCACC TCTTGAGGCA TCCCTTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTGATCTA TTGGGGAACA GAGAAGAGAC AGGCCACTAA GGTGAGGCTC 1939
TTTATATTAA GTTCCCCAGA GGAAGAGTAA GTTGAGAAGG TATCAGTTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTCCCT TCCCTCAGTA TTCTTCCTGG CAAGATAACC 2059
ATTAAGCATT TCGCCCAATCA GAATCTCATT TTATAGTTTT TCCCATTGGT CTTTAACTAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGGAGAA GACTTACTTC CTTCAGGGCA GCAGCCACAG CCAGGCTTCT GTCATACAGG 2239
TAGATCCCGA AGCACAGAGA CATAAAAAG GTCTCCCAGA AACTATAGA CCATTCTCCA 2299
AGTGGAATTC CCACCTAGG CTCTGGTCAC TAGATTGCAA CCTGTGTGTT TGTCAATCATC 2359
CTCATCTCAC CATTGTATTG CTATGCCCTC CCATAAAAAC ACATTGATCC CTAGCAAGAT 2419

FIG. 6G



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TATTGCATTC CAGATTTTAC TGCCTTTGCT AGGCTTTTGC TTAGCAAAGG GCTGACTTTC 2479
CATTGTTATC ATGGTGATA TATTTTGTG ACCATTCCCA CAAGTATACT TGATGTTGTC 2539
ATAGAACGAA CATCCTACTC TATGATTAC TAACCAATTA CTTTCCCAGA TCATAGACCT 2599
CTCTGCATAG TAGTCATAGG TCTTGACTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659
TATCTCCAAA GTCGAATGAG AAAGAACTCC AGCAAATCCA ATGGCTACAA ACTAAAAATC 2719
AGCATTATTT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTTTATT 2779
TTGAAAAAAA AAAAAAAA 2797

FIG. 6H



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GCGCGCGCGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGCTTT GGCTGAATCC 60
TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG 120
AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCCTC 180
TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAGCCT CCACCCAGCC ACATCTTGGG 240
AAAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60

FIG. 7A



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CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA	480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu	
65	70
	75
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA	528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val	
80	85
	90
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG	576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val	
95	100
	105
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC	624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val	
115	120
	125
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG	672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys	
130	135
	140
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG	720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu	
145	150
	155

FIG. 7B



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GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gly Leu His Gly His	
175 180 185 190	
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Thr Pro Arg	
210 215 220	
GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT	960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	

FIG. 7C



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CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	270
255	260
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	285
275	280
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Gly Glu Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	300
290	295
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	310
305	315
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	320
320	325
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Ile Leu	330
335	340
	345
	350

FIG. 7D



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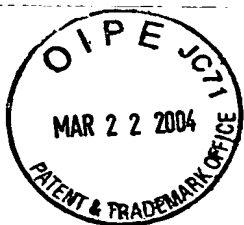
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AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG	1344
Lys Val Glu Asp Phe 355	
360	
365	
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC	1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr	
370	
375	
380	
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC	1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val	
385	
390	
395	
TTA CAG CTC ACA AAG AAA GTG AAG AAC ATA GAG ACG GGC TGG GCC TTG	1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu	
400	
405	
410	
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT	1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
415	
420	
425	
TGAGGCCACG TACTTCCTTG GAGACCTGCA TTGGCCAAACA CCTTTTAAAG GGGAGGAGAG	1590

FIG. 7E



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```
AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGAATT GAGCCTAGAG ATTAGGTTT 1650
AATTAATTTT ACACATCTAA TGTGAACTGC TGCCTAACCA CTCAAGAGTA CACAGCTGC 1710
ACCAGAGCAT CACAGAGAGC CCTGTGAGCC AAAAAGTATA GTTTTGAAC TTAACCTTG 1770
AGTGAGAGCC CAGGGACAGG TCCCTGGAAA CCAAAGAAAA ATCGCATTTT AACCCTTTGA 1830
GTGCCTCATT CCACTGAATA TTAAATTTT CCTCTTAAAT GTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAATATC AGTATTTTTT TCCTCCCTAT ACAGTGCCCT GCCCACCTT 1950
ATCTGCACCC ACCTCCCCTG AAAAAGAGAG AAAAAAAAAA AAAAAAAAA 1998
```

FIG. 7F



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CD39L2 1 MKKGIRYETSRKTSIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4 1 - - - - -
CD39L1 1 - - - - -
CD39L3 1 - - - - -
CD39 1 - - - - -

CD39L2 61 KWHRATATQAFFSITRAAPGARWQQAH-SPLGTAADGHEVFYGIMF
CD39L4 7 TVFFMLVVSCVCSAVSHRNQQTFEGIFLSSMCPINVSASTLYGIMF
CD39L1 1 - - - MAGKVRSLPPLLAAGLAGLLCVPTRDVREPALKYGIVL
CD39L3 16 KALYRTPTIIALVVLVSIVLSITVIQIHKQEVL-PPGLKYGIVL
CD39 7 SNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVL
ACR I

CD39L2 120 FT-RPPRETPTLTHETFKAVK-PGLSAYADDVEKSAQGIRELLDVAKQDIPFDFWKATPL
CD39L4 67 FVQKMPGQLPILEGEVFDSVK-PGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTPV
CD39L1 58 WPADKENDTGIVGQHSSCDVPGGISSYADNPSGASQSLVGCLEALQDVPKERHAGTPL
CD39L3 75 WPAEKENNTGVVSQTFKCSVKGSGISSYGNNPQDVPRAFECMQKVGQVPSHLHGSTPI
CD39 67 WPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPV
ACR II

FIG. 8A

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CD39L2	343	VSGQAAASLHELCAARVSEVLQNRVHRTEEVKHVDFFAFSYYDLAGVGLIDAEKGGG
CD39L4	290	YGGNQEGEVGFEPCEYAEVLRVVRGKLHQPEEVQRGSFYAFSYYDRAVDTDMDIDYEKGGI
CD39L1	283	PCTMAQRPNFNSSARVSLSGSSDPHLCDRLVSGLFSFSSC-PFSRCSFNGVFPQPPVAGN
CD39L3	307	LCTVDQRPESYNPNDVITFEGTGDPSSLCKEKVASIFDFKACHDQETCSFDGVYQPKIKGP
CD39	300	PCT--KRFEMTLPFQQFEIQIGIYQQCHQSILELFTSYC-PYSQCAFNGIFLPPPLQGD
CD39L2	403	LVVGDFEIAAKYVCRTELTQPQSSPFCMDLTYVSLLLQE-FGFPRSKVLKLTTRKIDNVE
CD39L4	350	LKVEDFERKAREVCNDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTCKVNNIE
CD39L1	342	FV-----AFSAFFYTVDLRTSMGLPVALQQLLEAAAVNCNQTTAQ-----
CD39L3	367	FV-----AFAGFYITASALNLSGSF---SLDTFNSSTNWFCSQNWSQLPLLKPKFDEVY
CD39	357	FG-----AFSAFYFVMKFLNLTS--EKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKY
CD39L2	462	TSWALGAI FHY IDSLSLNRQKSPAS*
CD39L4	410	TG WALGATFHL LQSLGISH
CD39L1	384	-----QLLSRGYGFDERAFGGVIFQKKAADTAVG WALGYMLNL TNLI PADPPG
CD39L3	418	ARSYCF SANYIYHLFVNGYKFT EETW PQIHFEKEVGNSSIAWSLGYMLSL TNQIPA ESPL
CD39	409	LSEYCF SGTYILSLLLQGYHFT AD SWEHIFHIGKIQGSDAGWTLGYMLNL TNMIPA EQP-

FIG. 8C



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CD39L2	485	
CD39L4	429	
CD39L1	432	<u>LRKGTDFSSWV</u> <u>LLLLLFASALLAALVLLLRQVHSAKLPSTI</u> *
CD39L3	478	<u>IRLP</u> <u>IEPPVFVGT</u> <u>LAF</u> <u>FTVAALLCLAF</u> <u>LAYLC</u> <u>SA</u> <u>TRRRKRHSEHAFD</u> <u>HAVDS</u> <u>D</u> *
CD39	468	<u>LSTPLSHSTYV</u> <u>FLMVLFSLV</u> <u>LV</u> <u>FTVA</u> <u>IIGLL</u> <u>IFHKKPSYFWKDMV</u> *

FIG. 8D

peaGDP	1	- - - - -	- - - - -	- - - - -	- - - - -	- M
potapyrase	1	- - - - -	- - - - -	- - - - -	- - - - -	M L N Q N
CD39L2	1	M K K G I R Y E T S R K T S Y I F Q Q P Q H G P W Q T R M R K I S N H G S L R V A K V A Y P L G L C V G V F I Y V A Y I				
CD39L4	1	- - - - -	- - - - -	- - - - -	- - - - -	- M A T S W G
dNTPase	1	- - - - -	- - - - -	- M K Y E Y K L L A T D E K P P R R K S S G S P N A S S G G N R Q P S G L		
YGD Pase	1	- - - - -	- - - - -	- - - - -	- - - - -	- K T P E
<div style="text-align: center;">ACRI ↑</div>						
peaGDP	2	E L L I K L I T F L L F S M P A I T S S Q Y L G N N L - L T S R K I F L K Q E E I S S Y A V V F	DAGSTGSR IHVY			
potapyrase	6	S H F I F I I L A I F L V L P L S L S K N V N A Q I - P L R R H L L S H E S E - - H Y A V I F	DAGSTGSR VHVF			
CD39L2	61	K W H R A T A T Q A F F S I T R A A P G A R W G Q Q A - H - S P L G T A A D G H E V F Y G I M F	DAGSTGTR VHVF			
CD39L4	7	T V F F M L V V S C V C S A V S H R N Q Q T W F E G I - F L S S M C P I N V S A S T L Y G I M F	DAGSTGTRI HVY			
dNTPase	37	K I S F L C L I I S V I L L F V F G F V S E N A S P - Y L A R L A S K F G Y S K V Q Y A A I I	DAGSTGSRVLAY			
YGD Pase	5	D I S I L P V N D E P G Y L Q D S K T E Q N Y P E L A D A V K S Q T S Q T C S E E H K Y V I M I	DAGSTGSRVIY			

FIG. 9A



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ACR II

peaGDP	61	<u>HFNQNLDDLHIGKGV</u> <u>YNNK</u> <u>ITPGLSSYANNPEQA</u> <u>AKSL</u> <u>IPLL</u> <u>LEQAEDVVPDDL</u> <u>QPK</u> <u>TPV</u>
potapyrase	63	<u>RFDEKLG</u> <u>LLPIGN</u> <u>IEYFM</u> <u>ATEPGLSSYAEDPKAAANSLEPLLDGAEGVVPQELQSE</u> <u>TPL</u>
CD39L2	119	<u>QFT-RPPRETPTL</u> <u>TH</u> <u>ETFKAVKPGLSAYADDVEKSAQGI</u> <u>REL</u> <u>LDVAKQDIPFD</u> <u>FWKAT</u> <u>PL</u>
CD39L4	66	<u>TFVQKMPGQLP</u> <u>ILEGEV</u> <u>FDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW</u> <u>KK</u> <u>TPV</u>
dNTPase	96	<u>KFNRSFIDNKKLVLYEELFKERKPGLS</u> <u>SFADNPAEGAHSIKLL</u> <u>DEARA</u> <u>FIPKEHWS</u> <u>STPL</u>
YGDPase	65	<u>KFD--VCTSPPTLLDEK</u> <u>FDMLEPGLSS</u> <u>FDTDSVGAANSLDPLLK</u> <u>VAMNYYPIKARS</u> <u>CTPV</u>

ACR III

peaGDP	121	<u>RLG</u> <u>ATAGLR</u> <u>LL</u> <u>NGDA</u> <u>SEKILQSV</u> <u>RDML</u> <u>SNRSTF</u> <u>-NVQPDAVSIID</u> <u>GT</u> <u>QEGSYLWVTVN</u> <u>VA</u>
potapyrase	123	<u>ELG</u> <u>ATAGLR</u> <u>ML</u> <u>KGDA</u> <u>AAEKILQAV</u> <u>RNLVKNQSTF</u> <u>-HSKDQWVTIL</u> <u>DDGT</u> <u>QEGSYMWAAIN</u> <u>YL</u>
CD39L2	178	<u>VLK</u> <u>ATAGLR</u> <u>LL</u> <u>PGEKAQKLLQK</u> <u>VKEVFK-ASPF-LVGDDC</u> <u>VSIMNGTDEG</u> <u>VS</u> <u>AWITIN</u> <u>FL</u>
CD39L4	126	<u>VLK</u> <u>ATAGLR</u> <u>LL</u> <u>PEHKAKALLFEVKEIFR-KSPF-LVPKGS</u> <u>VSIMDGSDEG</u> <u>IL</u> <u>AWVTVN</u> <u>FL</u>
dNTPase	156	<u>VLK</u> <u>ATAGLR</u> <u>LL</u> <u>PASKAENILNAVRDLFA-KSEF-SVDMDA</u> <u>VEIMDGTDEG</u> <u>IF</u> <u>SWFTVN</u> <u>FL</u>
YGDPase	123	<u>AVK</u> <u>ATAGLR</u> <u>LL</u> <u>GDAKSSKILSAVRDHL</u> <u>EKDYPFPVVEGDGVSIM</u> <u>GGDEEGVFAWITTT</u> <u>NYL</u>

FIG. 9B



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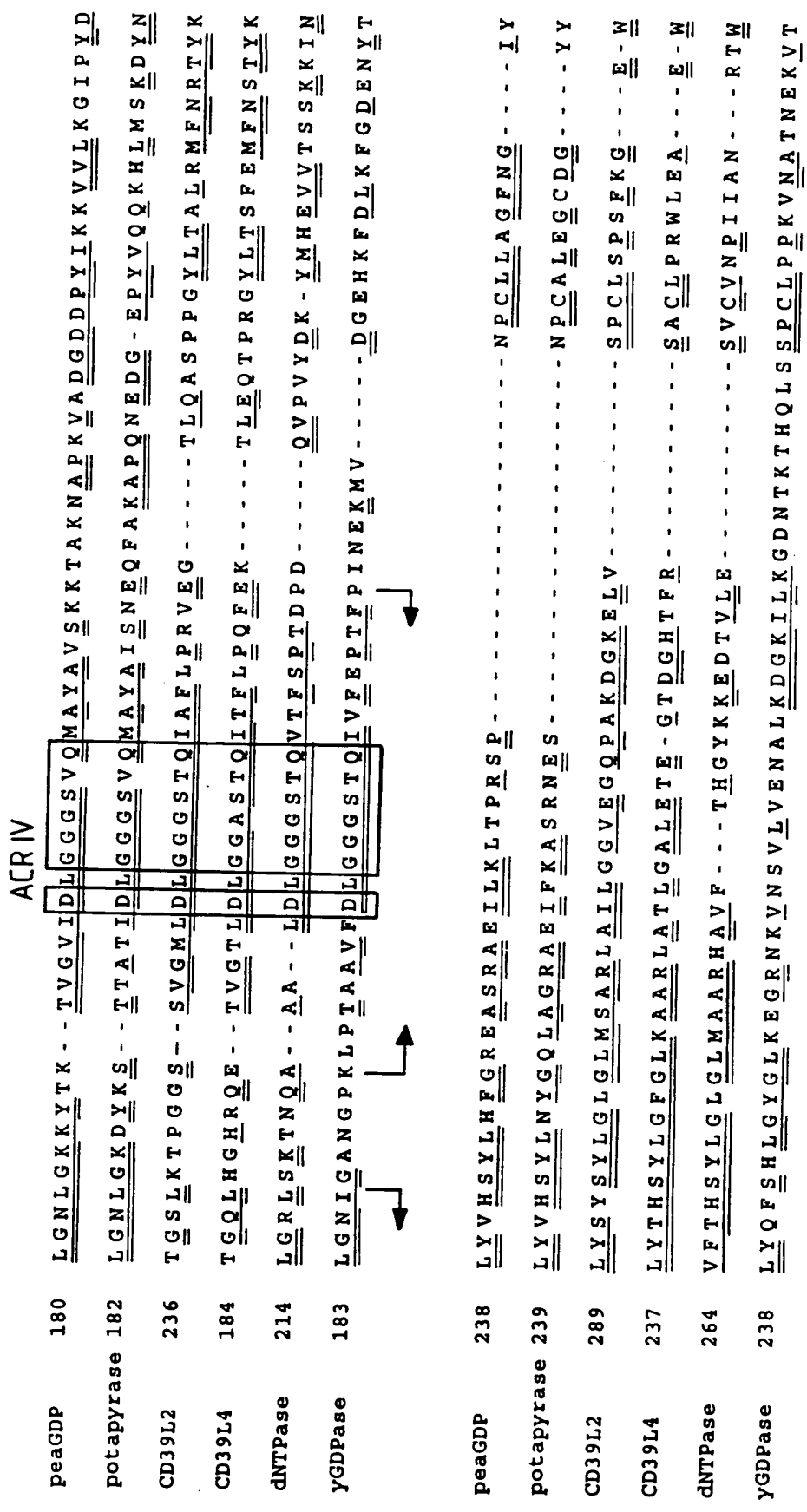


FIG. 9C



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peaGDP	276	<u>T</u> <u>Y</u> <u>S</u> <u>G</u> <u>E</u> <u>E</u> <u>F</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>Y</u> <u>T</u> <u>S</u> <u>G</u> <u>-</u> <u>A</u> <u>N</u> <u>F</u> <u>N</u> <u>K</u> <u>C</u> <u>K</u> <u>N</u> <u>T</u> <u>I</u> <u>R</u> <u>K</u> <u>A</u> <u>L</u> <u>K</u> <u>L</u> <u>N</u> <u>Y</u> <u>P</u> <u>C</u> <u>P</u> <u>Y</u> <u>Q</u> <u>N</u> <u>C</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>I</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>G</u> <u>G</u> <u>N</u> <u>G</u> <u>Q</u> <u>K</u> <u>N</u>
potapyrase	277	<u>S</u> <u>Y</u> <u>G</u> <u>G</u> <u>V</u> <u>D</u> <u>Y</u> <u>K</u> <u>V</u> <u>K</u> <u>A</u> <u>P</u> <u>K</u> <u>K</u> <u>G</u> <u>-</u> <u>S</u> <u>S</u> <u>W</u> <u>K</u> <u>R</u> <u>C</u> <u>R</u> <u>R</u> <u>L</u> <u>T</u> <u>R</u> <u>H</u> <u>A</u> <u>L</u> <u>K</u> <u>I</u> <u>N</u> <u>A</u> <u>K</u> <u>C</u> <u>N</u> <u>I</u> <u>E</u> <u>E</u> <u>C</u> <u>T</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>G</u> <u>G</u> <u>D</u> <u>G</u> <u>Q</u> <u>K</u> <u>N</u>
CD39L2	335	<u>E</u> <u>H</u> <u>A</u> <u>E</u> <u>V</u> <u>T</u> <u>Y</u> <u>R</u> <u>V</u> <u>S</u> <u>G</u> <u>Q</u> <u>K</u> <u>A</u> <u>A</u> <u>S</u> <u>L</u> <u>H</u> <u>E</u> <u>L</u> <u>C</u> <u>A</u> <u>A</u> <u>R</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>S</u> <u>E</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>Q</u> <u>N</u> <u>R</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>R</u> <u>T</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>E</u> <u>V</u> <u>K</u> <u>H</u> <u>V</u> <u>D</u>
CD39L4	282	<u>I</u> <u>F</u> <u>G</u> <u>G</u> <u>V</u> <u>K</u> <u>Y</u> <u>Q</u> <u>Y</u> <u>G</u> <u>G</u> <u>N</u> <u>Q</u> <u>E</u> <u>G</u> <u>E</u> <u>V</u> <u>G</u> <u>F</u> <u>E</u> <u>P</u> <u>C</u> <u>Y</u> <u>A</u> <u>E</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>L</u> <u>R</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>R</u> <u>G</u> <u>K</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>Q</u> <u>P</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>E</u> <u>V</u> <u>Q</u> <u>R</u> <u>G</u> <u>S</u>
dNTPase	308	<u>T</u> <u>Y</u> <u>G</u> <u>N</u> <u>V</u> <u>Q</u> <u>Y</u> <u>K</u> <u>V</u> <u>S</u> <u>G</u> <u>K</u> <u>E</u> <u>N</u> <u>G</u> <u>K</u> <u>S</u> <u>S</u> <u>A</u> <u>E</u> <u>Q</u> <u>I</u> <u>V</u> <u>D</u> <u>F</u> <u>D</u> <u>A</u> <u>C</u> <u>L</u> <u>E</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>K</u> <u>S</u> <u>K</u> <u>V</u> <u>M</u> <u>P</u> <u>L</u> <u>V</u> <u>K</u> <u>P</u> <u>K</u> <u>P</u> <u>-</u> <u>-</u> <u>-</u> <u>F</u> <u>T</u> <u>L</u> <u>K</u> <u>Q</u> <u>H</u> <u>A</u>
YGD Pase	298	<u>L</u> <u>E</u> <u>S</u> <u>K</u> <u>E</u> <u>T</u> <u>Y</u> <u>T</u> <u>I</u> <u>D</u> <u>F</u> <u>I</u> <u>G</u> <u>P</u> <u>D</u> <u>E</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>Q</u> <u>C</u> <u>R</u> <u>F</u> <u>L</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>L</u> <u>N</u> <u>K</u> <u>D</u> <u>A</u> <u>Q</u> <u>C</u> <u>Q</u> <u>S</u> <u>P</u> <u>C</u> <u>S</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>H</u> <u>Q</u> <u>P</u> <u>S</u> <u>L</u> <u>V</u> <u>R</u> <u>T</u> <u>F</u> <u>K</u> <u>E</u> <u>S</u> <u>N</u> <u>D</u>
peaGDP	332	<u>L</u> <u>F</u> <u>A</u> <u>S</u> <u>S</u> <u>S</u> <u>F</u> <u>F</u> <u>Y</u> <u>L</u> <u>P</u> <u>E</u> <u>D</u> <u>T</u> <u>G</u> <u>M</u> <u>V</u> <u>D</u> <u>A</u> <u>S</u> <u>T</u> <u>P</u> <u>N</u> <u>F</u> <u>I</u> <u>L</u> <u>R</u> <u>P</u> <u>V</u> <u>D</u> <u>I</u> <u>E</u> <u>T</u> <u>K</u> <u>A</u> <u>K</u> <u>E</u> <u>A</u> <u>C</u> <u>A</u> <u>L</u> <u>N</u> <u>F</u> <u>E</u> <u>D</u> <u>A</u> <u>K</u> <u>S</u> <u>T</u> <u>Y</u> <u>P</u> <u>F</u> <u>L</u> <u>D</u> <u>K</u> <u>K</u> <u>N</u> <u>V</u> <u>A</u> <u>S</u>
potapyrase	333	<u>I</u> <u>H</u> <u>A</u> <u>S</u> <u>S</u> <u>F</u> <u>F</u> <u>Y</u> <u>D</u> <u>I</u> <u>G</u> <u>A</u> <u>Q</u> <u>V</u> <u>G</u> <u>I</u> <u>V</u> <u>D</u> <u>T</u> <u>K</u> <u>F</u> <u>P</u> <u>S</u> <u>A</u> <u>L</u> <u>A</u> <u>K</u> <u>P</u> <u>I</u> <u>Q</u> <u>Y</u> <u>L</u> <u>N</u> <u>A</u> <u>A</u> <u>K</u> <u>V</u> <u>A</u> <u>C</u> <u>Q</u> <u>T</u> <u>N</u> <u>V</u> <u>A</u> <u>D</u> <u>I</u> <u>K</u> <u>S</u> <u>I</u> <u>F</u> <u>P</u> <u>K</u> <u>T</u> <u>Q</u> <u>D</u> <u>R</u> <u>N</u> <u>I</u> <u>-</u> <u>P</u>
CD39L2	379	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>G</u> <u>L</u> <u>I</u> <u>D</u> <u>A</u> <u>E</u> <u>-</u> <u>K</u> <u>G</u> <u>G</u> <u>S</u> <u>L</u> <u>V</u> <u>V</u> <u>G</u> <u>D</u> <u>F</u> <u>E</u> <u>I</u> <u>A</u> <u>A</u> <u>K</u> <u>Y</u> <u>V</u> <u>C</u> <u>R</u> <u>T</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>E</u> <u>T</u> <u>Q</u> <u>P</u> <u>Q</u> <u>S</u> <u>S</u> <u>P</u>
CD39L4	326	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>R</u> <u>A</u> <u>V</u> <u>D</u> <u>T</u> <u>D</u> <u>M</u> <u>I</u> <u>D</u> <u>Y</u> <u>E</u> <u>-</u> <u>K</u> <u>G</u> <u>G</u> <u>I</u> <u>L</u> <u>K</u> <u>V</u> <u>E</u> <u>D</u> <u>F</u> <u>E</u> <u>R</u> <u>K</u> <u>A</u> <u>R</u> <u>E</u> <u>V</u> <u>C</u> <u>D</u> <u>N</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>E</u> <u>N</u> <u>F</u> <u>T</u> <u>S</u> <u>G</u> <u>S</u> <u>P</u>
dNTPase	360	<u>V</u> <u>A</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>F</u> <u>E</u> <u>R</u> <u>A</u> <u>I</u> <u>E</u> <u>S</u> <u>G</u> <u>L</u> <u>V</u> <u>D</u> <u>P</u> <u>L</u> <u>-</u> <u>A</u> <u>G</u> <u>G</u> <u>E</u> <u>T</u> <u>T</u> <u>V</u> <u>E</u> <u>A</u> <u>Y</u> <u>R</u> <u>K</u> <u>K</u> <u>A</u> <u>Q</u> <u>E</u> <u>I</u> <u>C</u> <u>A</u> <u>I</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>P</u> <u>N</u> <u>D</u> <u>E</u> <u>-</u> <u>-</u> <u>-</u> <u>Q</u> <u>P</u>
YGD Pase	358	<u>I</u> <u>Y</u> <u>I</u> <u>F</u> <u>S</u> <u>Y</u> <u>F</u> <u>Y</u> <u>D</u> <u>R</u> <u>T</u> <u>R</u> <u>P</u> <u>L</u> <u>G</u> <u>M</u> <u>P</u> <u>L</u> <u>S</u> <u>F</u> <u>T</u> <u>L</u> <u>N</u> <u>E</u> <u>L</u> <u>N</u> <u>D</u> <u>L</u> <u>A</u> <u>R</u> <u>I</u> <u>V</u> <u>C</u> <u>K</u> <u>G</u> <u>E</u> <u>E</u> <u>T</u> <u>W</u> <u>N</u> <u>S</u> <u>V</u> <u>F</u> <u>S</u> <u>G</u> <u>I</u> <u>A</u> <u>G</u> <u>S</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>D</u> <u>E</u> <u>L</u> <u>E</u> <u>S</u> <u>D</u> <u>S</u>

FIG. 9D



peaGDP	392	<u>YV</u> <u>CMD</u> <u>LI</u> <u>YQ</u> <u>YV</u> <u>LL</u> <u>VD</u> <u>GF</u> <u>GL</u> <u>DP</u> <u>LQ</u> <u>KI</u> <u>TS</u> <u>GK</u> <u>EI</u> <u>EY</u> <u>QD</u> <u>AI</u> <u>VE</u> <u>AA</u> <u>WP</u> <u>LG</u> <u>NA</u> <u>VE</u> <u>AI</u> <u>SA</u> <u>LP</u> <u>KF</u> <u>ER</u> <u>L</u>
potapyrase	392	<u>YLC</u> <u>MD</u> <u>LI</u> <u>YE</u> <u>Y</u> <u>TLL</u> <u>VD</u> <u>GF</u> <u>GL</u> <u>NP</u> <u>HK</u> <u>EI</u> <u>TV</u> <u>I</u> <u>HD</u> <u>VQ</u> <u>YK</u> <u>NY</u> <u>LV</u> <u>GA</u> <u>AW</u> <u>PL</u> <u>GC</u> <u>AI</u> <u>DL</u> <u>VS</u> <u>ST</u> <u>TN</u> <u>KI</u> <u>RV</u>
CD39L2	428	<u>FSC</u> <u>MD</u> <u>LT</u> <u>YV</u> <u>SL</u> <u>LL</u> <u>QE</u> <u>-</u> <u>FG</u> <u>FP</u> <u>RS</u> <u>KV</u> <u>LK</u> <u>L</u> <u>TR</u> <u>KI</u> <u>DN</u> <u>-</u> <u>-</u> <u>-</u> <u>VET</u> <u>SW</u> <u>AL</u> <u>GA</u> <u>IF</u> <u>HY</u> <u>ID</u> <u>SL</u> <u>NR</u> <u>QK</u> <u>SP</u>
CD39L4	375	<u>FLC</u> <u>MD</u> <u>LS</u> <u>YI</u> <u>TA</u> <u>LL</u> <u>KD</u> <u>GF</u> <u>GF</u> <u>AD</u> <u>ST</u> <u>VL</u> <u>QL</u> <u>TK</u> <u>KV</u> <u>NN</u> <u>-</u> <u>-</u> <u>-</u> <u>IET</u> <u>GW</u> <u>AL</u> <u>GA</u> <u>TF</u> <u>HL</u> <u>LQ</u> <u>SL</u> <u>G</u> <u>ISH</u>
dNTPase	406	<u>FMC</u> <u>F</u> <u>D</u> <u>L</u> <u>T</u> <u>F</u> <u>I</u> <u>ST</u> <u>LL</u> <u>RE</u> <u>GF</u> <u>GL</u> <u>ND</u> <u>GK</u> <u>KI</u> <u>KL</u> <u>YK</u> <u>KI</u> <u>DG</u> <u>-</u> <u>-</u> <u>-</u> <u>HE</u> <u>IS</u> <u>WA</u> <u>LG</u> <u>CA</u> <u>YN</u> <u>VL</u> <u>TS</u> <u>DE</u> <u>KF</u> <u>SN</u> <u>S</u>
YGDPase	415	<u>HFC</u> <u>L</u> <u>D</u> <u>LS</u> <u>FQ</u> <u>VS</u> <u>LL</u> <u>HT</u> <u>GY</u> <u>DI</u> <u>PL</u> <u>Q</u> <u>RE</u> <u>LR</u> <u>TG</u> <u>KK</u> <u>IA</u> <u>NK</u> <u>-</u> <u>-</u> <u>-</u> <u>EI</u> <u>GW</u> <u>CL</u> <u>GA</u> <u>SL</u> <u>PL</u> <u>LL</u> <u>KA</u> <u>DN</u> <u>WK</u> <u>CK</u> <u>I</u>

peaGDP	452	<u>MY</u> <u>F</u> <u>V</u>
potapyrase	452	<u>AS</u> <u>S</u> <u>*</u>
CD39L2	483	<u>AS</u> <u>*</u>
CD39L4	429	
dNTPase	462	
YGDPase	471	<u>Q</u> <u>S</u> <u>A</u>

FIG. 9E